

## RAW SEQUENCE LISTING

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Application Serial Number: 10/809,075  
Source: 1FWO  
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IFWO

## RAW SEQUENCE LISTING

DATE: 03/09/2005

PATENT APPLICATION: US/10/809,075

TIME: 10:07:49

Input Set : A:\U0150863.ST25.txt

Output Set: N:\CRF4\03092005\J809075.raw

3 <110> APPLICANT: Dai, Ken-Shwo  
 5 <120> TITLE OF INVENTION: HUMAN RPS6KA6-RELATED GENE VARIANT ASSOCIATED WITH LUNG  
 CANCERS  
 7 <130> FILE REFERENCE: U 015086-3  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/809,075  
 C--> 10 <141> CURRENT FILING DATE: 2004-03-25  
 12 <160> NUMBER OF SEQ ID NOS: 8  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 2403  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Homo sapiens  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: (6)..(2099)  
 24 <223> OTHER INFORMATION:  
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 28 Met Leu Pro Phe Ala Pro Gln Asp Glu Pro Trp Asp Arg Glu Met  
 29 1 5 10 15  
 31 gaa gtg ttc agc ggc ggc ggc gcg agc agc ggc gag gta aat ggt ctt 98  
 32 Glu Val Phe Ser Gly Gly Gly Ala Ser Ser Gly Glu Val Asn Gly Leu  
 33 20 25 30  
 35 aaa atg gtt gat gag cca atg gaa gag gga gaa gca gat tct tgt cat 146  
 36 Lys Met Val Asp Glu Pro Met Glu Glu Gly Glu Ala Asp Ser Cys His  
 37 35 40 45  
 39 gat gaa gga gtt gtt aaa gaa atc cct att act cat cat gtt aag gaa 194  
 40 Asp Glu Gly Val Val Lys Glu Ile Pro Ile Thr His His Val Lys Glu  
 41 50 55 60  
 43 ggc tat gag aaa gca gat cct gca cag ttt gag ttg ctc aag gtt ctt 242  
 44 Gly Tyr Glu Lys Ala Asp Pro Ala Gln Phe Glu Leu Leu Lys Val Leu  
 45 65 70 75  
 47 ggt cag ggg tca ttt gga aag gtt ttt ctt gtt aga aag aag acc ggt 290  
 48 Gly Gln Gly Ser Phe Gly Lys Val Phe Leu Val Arg Lys Lys Thr Gly  
 49 80 85 90 95  
 51 cct gat gct ggg cag ctc tat gca atg aag gtg tta aaa aaa gcc tct 338  
 52 Pro Asp Ala Gly Gln Leu Tyr Ala Met Lys Val Leu Lys Lys Ala Ser  
 53 100 105 110  
 55 tta aaa gtt cga gac aga gtt cgg aca aag atg gag agg gat ata ctg 386  
 56 Leu Lys Val Arg Asp Arg Val Arg Thr Lys Met Glu Arg Asp Ile Leu  
 57 115 120 125  
 59 gtg gaa gta aat cat cca ttt att gtc aaa ttg cac tat gcc ttt cag 434  
 60 Val Glu Val Asn His Pro Phe Ile Val Lys Leu His Tyr Ala Phe Gln  
 61 130 135 140

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63	act	gaa	ggg	aaa	ctg	tac	tta	ata	ctg	gat	ttt	ctc	agg	gga	gga	gat	482
64	Thr	Glu	Gly	Lys	Leu	Tyr	Leu	Ile	Leu	Asp	Phe	Leu	Arg	Gly	Gly	Asp	
65		145					150				155						
67	gtt	ttc	aca	aga	tta	tcc	aaa	gag	gtt	ctg	ttt	aca	gag	gaa	gat	gtg	530
68	Val	Phe	Thr	Arg	Leu	Ser	Lys	Glu	Val	Leu	Phe	Thr	Glu	Glu	Asp	Val	
69	160				165					170					175		
71	aaa	ttc	tac	ctc	gca	gaa	ctg	gcc	ctt	gct	ttg	gat	cat	ctg	cac	caa	578
72	Lys	Phe	Tyr	Leu	Ala	Glu	Leu	Ala	Leu	Ala	Leu	Asp	His	Leu	His	Gln	
73				180					185				190				
75	tta	gga	att	gtt	tat	aga	gac	ctg	aag	cca	gaa	aac	att	ttg	ctt	gat	626
76	Leu	Gly	Ile	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	
77			195					200				205					
79	gaa	ata	gga	cat	atc	aaa	tta	aca	gat	ttt	gga	ctc	agc	aag	gag	tca	674
80	Glu	Ile	Gly	His	Ile	Lys	Leu	Thr	Asp	Phe	Gly	Leu	Ser	Lys	Glu	Ser	
81		210					215				220						
83	gta	gat	caa	gaa	aag	aag	gct	tac	tca	ttt	tgt	ggg	aca	gta	gag	tat	722
84	Val	Asp	Gln	Glu	Lys	Lys	Ala	Tyr	Ser	Phe	Cys	Gly	Thr	Val	Glu	Tyr	
85		225				230					235						
87	atg	gct	cct	gaa	gta	gta	aat	agg	aga	ggc	cat	tcc	cag	agt	gct	gat	770
88	Met	Ala	Pro	Glu	Val	Val	Asn	Arg	Arg	Gly	His	Ser	Gln	Ser	Ala	Asp	
89	240				245				250				255				
91	tgg	tgg	tca	tat	ggg	gtt	ctt	atg	ttt	gaa	atg	ctt	act	ggg	act	ctg	818
92	Trp	Trp	Ser	Tyr	Gly	Val	Leu	Met	Phe	Glu	Met	Leu	Thr	Gly	Thr	Leu	
93			260					265				270					
95	cca	ttt	caa	ggg	aaa	gac	aga	aat	gag	acc	atg	aat	atg	ata	tta	aaa	866
96	Pro	Phe	Gln	Gly	Lys	Asp	Arg	Asn	Glu	Thr	Met	Asn	Met	Ile	Leu	Lys	
97			275				280				285						
99	gca	aaa	ctt	gga	atg	cct	caa	ttt	ctt	agt	gct	gaa	gca	caa	agt	ctt	914
100	Ala	Lys	Leu	Gly	Met	Pro	Gln	Phe	Leu	Ser	Ala	Glu	Ala	Gln	Ser	Leu	
101		290					295				300						
103	cta	agg	atg	tta	ttc	aaa	agg	aat	cca	gca	aat	aga	ttg	gga	tca	gaa	962
104	Leu	Arg	Met	Leu	Phe	Lys	Arg	Asn	Pro	Ala	Asn	Arg	Leu	Gly	Ser	Glu	
105		305				310					315						
107	gga	gtt	gaa	gaa	atc	aaa	aga	cat	ctg	ttt	ttt	gca	aat	att	gac	tgg	1010
108	Gly	Val	Glu	Glu	Ile	Lys	Arg	His	Leu	Phe	Phe	Ala	Asn	Ile	Asp	Trp	
109	320				325					330			335				
111	gat	aaa	tta	tat	aaa	aga	gaa	gtt	caa	cct	cct	ttc	aaa	cct	gct	tct	1058
112	Asp	Lys	Leu	Tyr	Lys	Arg	Glu	Val	Gln	Pro	Pro	Phe	Lys	Pro	Ala	Ser	
113			340					345				350					
115	gga	aaa	cca	gat	gat	act	ttt	tgt	ttt	gat	cct	gaa	ttt	act	gca	aaa	1106
116	Gly	Lys	Pro	Asp	Asp	Thr	Phe	Cys	Phe	Asp	Pro	Glu	Phe	Thr	Ala	Lys	
117			355					360				365					
119	aca	cct	aaa	gat	tct	ccc	ggg	ttg	cca	gcc	agt	gca	aat	gct	cat	cag	1154
120	Thr	Pro	Lys	Asp	Ser	Pro	Gly	Leu	Pro	Ala	Ser	Ala	Asn	Ala	His	Gln	
121			370				375					380					
123	ctc	ttc	aaa	gga	ttc	agc	ttt	gtt	gca	act	tct	att	gca	gaa	gaa	tat	1202
124	Leu	Phe	Lys	Gly	Phe	Ser	Phe	Val	Ala	Thr	Ser	Ile	Ala	Glu	Glu	Tyr	
125		385				390					395						
127	aaa	atc	act	cct	atc	aca	agt	gca	aat	gta	tta	cca	att	gtt	cag	ata	1250

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129	400					405					410					415	
131	aat	gga	aat	gct	gca	caa	ttt	ggg	gaa	gta	tat	gaa	ttg	aag	gag	gat	1298
132	Asn	Gly	Asn	Ala	Ala	Gln	Phe	Gly	Glu	Val	Tyr	Glu	Leu	Lys	Glu	Asp	
133					420					425					430		
135	att	ggg	gtt	ggc	tcc	tac	tct	gtt	tgc	aag	cga	tgc	ata	cat	gca	act	1346
136	Ile	Gly	Val	Gly	Ser	Tyr	Ser	Val	Cys	Lys	Arg	Cys	Ile	His	Ala	Thr	
137				435					440					445			
139	acc	aac	atg	gaa	ttt	gca	gtg	aag	atc	att	gac	aaa	agt	aag	cga	gac	1394
140	Thr	Asn	Met	Glu	Phe	Ala	Val	Lys	Ile	Ile	Asp	Lys	Ser	Lys	Arg	Asp	
141			450					455					460				
143	cct	tca	gaa	gag	att	gaa	ata	ttg	atg	cgc	tat	gga	caa	cat	ccc	aac	1442
144	Pro	Ser	Glu	Glu	Ile	Glu	Ile	Leu	Met	Arg	Tyr	Gly	Gln	His	Pro	Asn	
145		465					470					475					
147	att	att	act	ttg	aag	gat	gtc	ttt	gat	gat	ggg	aga	tat	gtt	tac	ctt	1490
148	Ile	Ile	Thr	Leu	Lys	Asp	Val	Phe	Asp	Asp	Gly	Arg	Tyr	Val	Tyr	Leu	
149	480				485					490					495		
151	gtt	acg	gat	tta	atg	aaa	gga	gga	gag	tta	ctt	gac	cgt	att	ctc	aaa	1538
152	Val	Thr	Asp	Leu	Met	Lys	Gly	Gly	Glu	Leu	Asp	Arg	Ile	Leu	Lys		
153				500					505					510			
155	caa	aaa	tgt	ttc	tcg	gaa	cgg	gag	gct	agt	gat	ata	cta	tat	gta	ata	1586
156	Gln	Lys	Cys	Phe	Ser	Glu	Arg	Glu	Ala	Ser	Asp	Ile	Leu	Tyr	Val	Ile	
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159	agt	aag	aca	gtt	gac	tat	ctt	cat	tgt	caa	gga	gtt	gtt	cat	cgt	gat	1634
160	Ser	Lys	Thr	Val	Asp	Tyr	Leu	His	Cys	Gln	Gly	Val	Val	His	Arg	Asp	
161			530				535						540				
163	ctt	aaa	cct	agt	aat	att	tta	tac	atg	gat	gaa	tca	gcc	agt	gca	gat	1682
164	Leu	Lys	Pro	Ser	Asn	Ile	Leu	Tyr	Met	Asp	Glu	Ser	Ala	Ser	Ala	Asp	
165		545				550					555						
167	tca	atc	agg	ata	tgt	gat	ttt	ggg	ttt	gca	aaa	caa	ctt	cga	gga	gaa	1730
168	Ser	Ile	Arg	Ile	Cys	Asp	Phe	Gly	Phe	Ala	Lys	Gln	Leu	Arg	Gly	Glu	
169	560				565					570					575		
171	aat	gga	ctt	ctc	tta	act	cca	tgc	tac	act	gca	aac	ttt	gtt	gca	cct	1778
172	Asn	Gly	Leu	Leu	Leu	Thr	Pro	Cys	Tyr	Thr	Ala	Asn	Phe	Val	Ala	Pro	
173				580					585					590			
175	gag	gtt	ctt	atg	caa	cag	gga	tat	gat	gct	gct	tgt	gat	atc	tgg	agt	1826
176	Glu	Val	Leu	Met	Gln	Gln	Gly	Tyr	Asp	Ala	Ala	Cys	Asp	Ile	Trp	Ser	
177				595				600					605				
179	tta	gga	gtc	ctt	ttt	tac	aca	atg	ttg	gct	ggc	tac	act	cca	ttt	gct	1874
180	Leu	Gly	Val	Leu	Phe	Tyr	Thr	Met	Leu	Ala	Gly	Tyr	Thr	Pro	Phe	Ala	
181			610					615					620				
183	aat	ggc	ccc	aat	gat	act	cct	gaa	gag	ata	ctg	ctg	cgt	ata	ggc	aat	1922
184	Asn	Gly	Pro	Asn	Asp	Thr	Pro	Glu	Glu	Ile	Leu	Leu	Arg	Ile	Gly	Asn	
185		625				630					635						
187	gga	aaa	ttc	tct	ttg	agt	ggg	gga	aac	tgg	gac	aat	att	tca	gac	gga	1970
188	Gly	Lys	Phe	Ser	Leu	Ser	Gly	Gly	Asn	Trp	Asp	Asn	Ile	Ser	Asp	Gly	
189	640				645					650				655			
191	gca	aag	gga	gca	atg	gtt	gca	aca	tac	tct	gcc	ctg	act	cac	aag	acc	2018
192	Ala	Lys	Gly	Ala	Met	Val	Ala	Thr	Tyr	Ser	Ala	Leu	Thr	His	Lys	Thr	

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197          675          680          685
199 cgg agc atg aaa aag cga aca tca act ggc ctg taagatttgt ggtgttccta      2119
200 Arg Ser Met Lys Lys Arg Thr Ser Thr Gly Leu
201          690          695
203 ggccaaactg gatgaagatg aaattaaatg tgtggcctttt ttctatttct tatcaaaggc      2179
205 atcgttgtct gctaaattac ttgaatatta agtaatatta aatccccatt tttaggggaa      2239
207 gtgagattta aaaaaccatt cacaggtcca caatattcat actatgtgtt tgcagtagtg      2299
209 ttcaagtgtt tatttaagca tataattggt gtccaccagg tcctcacaac ttctctgcac      2359
211 acaagcttct aaaattcctt tcaaataaag ttactttaat attt      2403
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215 <211> LENGTH: 698
216 <212> TYPE: PRT
217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 2
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225 Val Phe Ser Gly Gly Gly Ala Ser Ser Gly Glu Val Asn Gly Leu Lys
226          20          25          30
229 Met Val Asp Glu Pro Met Glu Glu Gly Glu Ala Asp Ser Cys His Asp
230          35          40          45
233 Glu Gly Val Val Lys Glu Ile Pro Ile Thr His His Val Lys Glu Gly
234          50          55          60
237 Tyr Glu Lys Ala Asp Pro Ala Gln Phe Glu Leu Leu Lys Val Leu Gly
238 65          70          75          80
241 Gln Gly Ser Phe Gly Lys Val Phe Leu Val Arg Lys Lys Thr Gly Pro
242          85          90          95
245 Asp Ala Gly Gln Leu Tyr Ala Met Lys Val Leu Lys Lys Ala Ser Leu
246          100          105          110
249 Lys Val Arg Asp Arg Val Arg Thr Lys Met Glu Arg Asp Ile Leu Val
250          115          120          125
253 Glu Val Asn His Pro Phe Ile Val Lys Leu His Tyr Ala Phe Gln Thr
254          130          135          140
257 Glu Gly Lys Leu Tyr Leu Ile Leu Asp Phe Leu Arg Gly Gly Asp Val
258 145          150          155          160
261 Phe Thr Arg Leu Ser Lys Glu Val Leu Phe Thr Glu Glu Asp Val Lys
262          165          170          175
265 Phe Tyr Leu Ala Glu Leu Ala Leu Ala Leu Asp His Leu His Gln Leu
266          180          185          190
269 Gly Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu
270          195          200          205
273 Ile Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Glu Ser Val
274          210          215          220
277 Asp Gln Glu Lys Lys Ala Tyr Ser Phe Cys Gly Thr Val Glu Tyr Met
278 225          230          235          240
281 Ala Pro Glu Val Val Asn Arg Arg Gly His Ser Gln Ser Ala Asp Trp
282          245          250          255

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285 Trp Ser Tyr Gly Val Leu Met Phe Glu Met Leu Thr Gly Thr Leu Pro
286           260           265           270
289 Phe Gln Gly Lys Asp Arg Asn Glu Thr Met Asn Met Ile Leu Lys Ala
290           275           280           285
293 Lys Leu Gly Met Pro Gln Phe Leu Ser Ala Glu Ala Gln Ser Leu Leu
294           290           295           300
297 Arg Met Leu Phe Lys Arg Asn Pro Ala Asn Arg Leu Gly Ser Glu Gly
298 305           310           315           320
301 Val Glu Glu Ile Lys Arg His Leu Phe Phe Ala Asn Ile Asp Trp Asp
302           325           330           335
305 Lys Leu Tyr Lys Arg Glu Val Gln Pro Pro Phe Lys Pro Ala Ser Gly
306           340           345           350
309 Lys Pro Asp Asp Thr Phe Cys Phe Asp Pro Glu Phe Thr Ala Lys Thr
310           355           360           365
313 Pro Lys Asp Ser Pro Gly Leu Pro Ala Ser Ala Asn Ala His Gln Leu
314           370           375           380
317 Phe Lys Gly Phe Ser Phe Val Ala Thr Ser Ile Ala Glu Glu Tyr Lys
318 385           390           395           400
321 Ile Thr Pro Ile Thr Ser Ala Asn Val Leu Pro Ile Val Gln Ile Asn
322           405           410           415
325 Gly Asn Ala Ala Gln Phe Gly Glu Val Tyr Glu Leu Lys Glu Asp Ile
326           420           425           430
329 Gly Val Gly Ser Tyr Ser Val Cys Lys Arg Cys Ile His Ala Thr Thr
330           435           440           445
333 Asn Met Glu Phe Ala Val Lys Ile Ile Asp Lys Ser Lys Arg Asp Pro
334           450           455           460
337 Ser Glu Glu Ile Glu Ile Leu Met Arg Tyr Gly Gln His Pro Asn Ile
338 465           470           475           480
341 Ile Thr Leu Lys Asp Val Phe Asp Asp Gly Arg Tyr Val Tyr Leu Val
342           485           490           495
345 Thr Asp Leu Met Lys Gly Gly Glu Leu Leu Asp Arg Ile Leu Lys Gln
346           500           505           510
349 Lys Cys Phe Ser Glu Arg Glu Ala Ser Asp Ile Leu Tyr Val Ile Ser
350           515           520           525
353 Lys Thr Val Asp Tyr Leu His Cys Gln Gly Val Val His Arg Asp Leu
354           530           535           540
357 Lys Pro Ser Asn Ile Leu Tyr Met Asp Glu Ser Ala Ser Ala Asp Ser
358 545           550           555           560
361 Ile Arg Ile Cys Asp Phe Gly Phe Ala Lys Gln Leu Arg Gly Glu Asn
362           565           570           575
365 Gly Leu Leu Leu Thr Pro Cys Tyr Thr Ala Asn Phe Val Ala Pro Glu
366           580           585           590
369 Val Leu Met Gln Gln Gly Tyr Asp Ala Ala Cys Asp Ile Trp Ser Leu
370           595           600           605
373 Gly Val Leu Phe Tyr Thr Met Leu Ala Gly Tyr Thr Pro Phe Ala Asn
374           610           615           620
377 Gly Pro Asn Asp Thr Pro Glu Glu Ile Leu Leu Arg Ile Gly Asn Gly
378 625           630           635           640
381 Lys Phe Ser Leu Ser Gly Gly Asn Trp Asp Asn Ile Ser Asp Gly Ala

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:24

L:407 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:405